

ACC TAC TGT TTC CTA GTC TTT GCT ACA ATT TGT ATC ACA GGT GCT ATC Thr Tyr Cys Phe Leu Val Phe Ala Thr Ile Cys Ile Thr Gly Ala Ile 480 485 490	1551
TAC CTG TAT TTT GTG CTG CCT GAG ACC AAA AAC AGA ACC TAT GCA GAA Tyr Leu Tyr Phe Val Leu Pro Glu Thr Lys Asn Arg Thr Tyr Ala Glu 495 500 505	1599
ATC AGC CAG GCA TTT TCC AAA AGG AAC AAA GCA TAC CCA CCA GAA GAG Ile Ser Gln Ala Phe Ser Lys Arg Asn Lys Ala Tyr Pro Pro Glu Glu 510 515 520 525	1647
AAA ATC GAC TCA GCT GTC ACT GAT GCT CCT GCT TCT TCT CCT TTC ACT Lys Ile Asp Ser Ala Val Thr Asp Ala Pro Ala Ser Ser Pro Phe Thr 530 535 540	1695
ACT CCG AAT ACA GCC TGG ATT CAA GCT GCC GCC ACC ACC ACC GCC ACC Thr Pro Asn Thr Ala Trp Ile Gln Ala Ala Thr Thr Thr Ala Thr 545 550 555	1743
AAA AAA GAA CAC CCA TTG TAAACGGTCA TGTGGTATTT CCTCAACCTG GAATGACC Lys Lys Glu His Pro Leu 560	1799
TTCCCTATC TTCTTCTCCT GGAGAACACC AAGTCATGAT GTCAGACAAG AGCTTGGATT TTGGAGACAT GGGTTTGAAT TCCAGTCATT CATTCTTTTA TTCAGCAAAT ATTTAACAAG TACTGACATG TCCCATATGT TGTTTTACCC ACTGGTTATA CAATGGGAGG GAGAGAGAGA GAGAGAGAGA GAGAGAGATG CTATTCTAAA AGCTTGAAGT CTAGGCTGTG CACGGTGGCT CACGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGTGGGT GGATCGTGAG GTCAGGAGAT TGAGACCATC CTGGCTAACA TGGTGAAACT CCCTCTCTAC TAAAAATACA AAAAATTAGC TGAGCATGGT GGCGGGCGCC TGTAGTCCCA GCTACTTGGG AGGCTGAGGC AGGAGAATGG CGTGAACCCA GGAGGCGGAG CTTGCAGTGA GCCGAGATCA CACCACCACA CTCCAGCCTG GGTGACAGAG CCAGACTCCG TCTCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGGGCGG CCGC	1859 1919 1979 2039 2099 2159 2219 2279 2339 2343

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Arg	Lys	Gln	Asn	Arg	Asn	Ser	Lys	Glu	Leu	Gly	Leu	Val	Pro
1				5					10					15	
Leu	Thr	Asp	Asp	Thr	Ser	His	Ala	Gly	Pro	Pro	Gly	Pro	Gly	Arg	Ala
		20						25					30		
Leu	Leu	Glu	Cys	Asp	His	Leu	Arg	Ser	Gly	Val	Pro	Gly	Gly	Arg	Arg
		35					40					45			
Arg	Lys	Asp	Trp	Ser	Cys	Ser	Leu	Leu	Val	Ala	Ser	Leu	Ala	Gly	Ala
		50				55					60				
Phe	Gly	Ser	Ser	Phe	Leu	Tyr	Gly	Tyr	Asn	Leu	Ser	Val	Val	Asn	Ala
		65			70				75					80	
Pro	Thr	Pro	Tyr	Ile	Lys	Ala	Phe	Tyr	Asn	Glu	Ser	Trp	Glu	Arg	Arg
			85					90						95	
His	Gly	Arg	Pro	Ile	Asp	Pro	Asp	Thr	Leu	Thr	Leu	Leu	Trp	Ser	Val
			100					105					110		

Thr	Val	Ser	Ile	Phe	Ala	Ile	Gly	Gly	Leu	Val	Gly	Thr	Leu	Ile	Val
		115					120					125			
Lys	Met	Ile	Gly	Lys	Val	Leu	Gly	Arg	Lys	His	Thr	Leu	Leu	Ala	Asn
	130					135					140				
Asn	Gly	Phe	Ala	Ile	Ser	Ala	Ala	Leu	Leu	Met	Ala	Cys	Ser	Leu	Gln
145					150					155					160
Ala	Gly	Ala	Phe	Glu	Met	Leu	Ile	Val	Gly	Arg	Phe	Ile	Met	Gly	Ile
				165					170					175	
Asp	Gly	Gly	Val	Ala	Leu	Ser	Val	Leu	Pro	Met	Tyr	Leu	Ser	Glu	Ile
			180					185					190		
Ser	Pro	Lys	Glu	Ile	Arg	Gly	Ser	Leu	Gly	Gln	Val	Thr	Ala	Ile	Phe
		195					200					205			
Ile	Cys	Ile	Gly	Val	Phe	Thr	Gly	Gln	Leu	Leu	Gly	Leu	Pro	Glu	Leu
	210					215					220				
Leu	Gly	Lys	Glu	Ser	Thr	Trp	Pro	Tyr	Leu	Phe	Gly	Val	Ile	Val	Val
225					230					235					240
Pro	Ala	Val	Val	Gln	Leu	Leu	Ser	Leu	Pro	Phe	Leu	Pro	Asp	Ser	Pro
				245					250					255	
Arg	Tyr	Leu	Leu	Glu	Lys	His	Asn	Glu	Ala	Arg	Ala	Val	Lys	Ala	
			260				265						270		
Phe	Gln	Thr	Phe	Leu	Gly	Lys	Ala	Asp	Val	Ser	Gln	Glu	Val	Glu	Glu
		275					280					285			
Val	Leu	Ala	Glu	Ser	His	Val	Gln	Arg	Ser	Ile	Arg	Leu	Val	Ser	Val
	290					295					300				
Leu	Glu	Leu	Leu	Arg	Ala	Pro	Tyr	Val	Arg	Trp	Gln	Val	Val	Thr	Val
305					310					315					320
Ile	Val	Thr	Met	Ala	Cys	Tyr	Gln	Leu	Cys	Gly	Leu	Asn	Ala	Ile	Trp
			325						330					335	
Phe	Tyr	Thr	Asn	Ser	Ile	Phe	Gly	Lys	Ala	Gly	Ile	Pro	Pro	Ala	Lys
			340					345					350		
Ile	Pro	Tyr	Val	Thr	Leu	Ser	Thr	Gly	Gly	Ile	Glu	Thr	Leu	Ala	Ala
		355					360					365			
Val	Phe	Ser	Gly	Leu	Val	Ile	Glu	His	Leu	Gly	Arg	Arg	Pro	Leu	Leu
	370					375					380				
Ile	Gly	Gly	Phe	Gly	Leu	Met	Gly	Leu	Phe	Phe	Gly	Thr	Leu	Thr	Ile
385					390					395					400
Thr	Leu	Thr	Leu	Gln	Asp	His	Ala	Pro	Trp	Val	Pro	Tyr	Leu	Ser	Ile
				405					410					415	
Val	Gly	Ile	Leu	Ala	Ile	Ile	Ala	Ser	Phe	Cys	Ser	Gly	Pro	Gly	Gly
			420					425					430		
Ile	Pro	Phe	Ile	Leu	Thr	Gly	Glu	Phe	Phe	Gln	Gln	Ser	Gln	Arg	Pro
		435					440						445		
Ala	Ala	Phe	Ile	Ile	Ala	Gly	Thr	Val	Asn	Trp	Leu	Ser	Asn	Phe	Ala
	450					455					460				
Val	Gly	Leu	Leu	Phe	Pro	Phe	Ile	Gln	Lys	Ser	Leu	Asp	Thr	Tyr	Cys
465					470					475					480
Phe	Leu	Val	Phe	Ala	Thr	Ile	Cys	Ile	Thr	Gly	Ala	Ile	Tyr	Leu	Tyr
				485					490					495	
Phe	Val	Leu	Pro	Glu	Thr	Lys	Asn	Arg	Thr	Tyr	Ala	Glu	Ile	Ser	Gln
			500					505					510		
Ala	Phe	Ser	Lys	Arg	Asn	Lys	Ala	Tyr	Pro	Pro	Glu	Glu	Lys	Ile	Asp
		515					520					525			
Ser	Ala	Val	Thr	Asp	Ala	Pro	Ala	Ser	Ser	Pro	Phe	Thr	Thr	Pro	Asn
	530					535					540				
Thr	Ala	Trp	Ile	Gln	Ala	Ala	Ala	Thr	Thr	Thr	Ala	Thr	Lys	Lys	Glu
545					550					555					560
His	Pro	Leu													

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Gly	Phe	Ser	Lys	Leu	Gly	Lys	Ser	Phe	Glu	Met	Leu	Ile	Leu	Gly
1				5					10					15	
Arg	Phe	Ile	Ile	Gly	Val	Tyr	Cys	Gly	Leu	Thr	Thr	Gly	Phe	Val	Pro
			20					25					30		
Met	Tyr	Val	Gly	Glu	Val	Ser	Pro	Thr	Glu	Leu	Arg	Gly	Ala	Leu	Gly
			35				40						45		
Thr	Leu	His	Gln	Leu	Gly	Ile	Val	Val	Gly	Ile	Leu	Ile	Ala	Gln	Val
						55					60				
Phe	Gly	Leu	Asp	Ser	Ile	Met	Gly	Asn	Gln	Glu	Leu	Trp	Pro	Leu	Leu
65					70					75				80	
Leu	Ser	Val	Ile	Phe	Ile	Pro	Ala	Leu	Leu	Gln	Cys	Ile	Leu	Leu	Pro
				85					90					95	
Phe	Cys	Pro	Glu	Ser	Pro	Arg	Phe	Leu	Leu	Ile	Asn	Arg	Asn	Glu	Glu
				100				105					110		
Asn	Arg	Ala	Lys	Ser	Val	Leu	Lys	Lys	Leu	Arg	Gly	Thr	Ala	Asp	Val
							120					125			
Thr	Arg	Asp	Leu	Gln	Glu	Met	Lys	Glu	Glu	Ser	Arg	Gln	Met	Met	Arg
						135					140				
Glu	Lys	Lys	Val	Thr	Ile	Leu	Glu	Leu	Phe	Arg	Ser	Ala	Ala	Tyr	Arg
145					150					155				160	
Gln	Pro	Ile	Leu	Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser
				165					170					175	
Gly	Ile	Asn	Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Lys	Ala
				180				185					190		
Gly	Val	Gln	Gln	Pro	Val	Tyr	Ala	Thr	Ile	Gly	Ser	Gly	Ile	Val	Asn
				195			200					205			
Thr	Ala	Phe	Thr	Val	Val	Ser	Leu	Phe	Val	Val	Glu	Arg	Ala	Gly	Arg
						215					220				
Arg	Thr	Leu	His	Leu	Ile	Gly	Leu	Ala	Gly	Met	Ala	Gly	Cys	Ala	Val
225					230					235				240	
Leu	Met	Thr	Ile	Ala	Leu	Ala	Leu	Leu	Glu	Gln	Leu	Pro	Trp	Met	Ser
				245					250					255	
Tyr	Leu	Ser	Ile	Val	Ala	Ile	Phe	Gly	Phe	Val	Ala	Phe	Phe	Glu	Val
				260				265					270		
Gly	Pro	Gly	Pro	Ile	Pro	Trp	Phe	Ile	Val	Ala	Glu	Leu	Phe	Ser	Gln
				275				280				285			
Gly	Pro	Arg	Pro	Ala	Ala	Ile	Ala	Val	Ala	Gly	Phe	Ser	Asn	Trp	Thr
				290			295				300				
Ser	Asn	Phe	Ile	Val	Gly	Met	Cys	Phe	Gln	Tyr	Val	Glu	Gln	Leu	Cys
305					310					315				320	
Gly	Pro	Tyr	Val	Phe	Ile	Ile	Phe	Thr	Val	Leu	Leu	Val	Leu	Phe	Phe
				325					330					335	
Ile	Phe	Thr	Tyr	Phe	Lys	Val	Pro	Glu	Thr	Lys	Gly	Arg	Thr	Phe	Asp
				340				345					350		
Glu	Ile	Ala	Ser	Gly	Phe	Arg	Gln	Gly	Gly	Ala	Ser	Gln	Ser	Asp	Lys
				355			360					365			
Thr	Pro	Glu	Glu	Leu	Phe	His	Pro	Leu	Gly	Ala	Asp	Ser	Gln	Val	
370					375						380				

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear